

1 GGCACGAGGT CCCCCGACGCG CCCCCGCCAA CCCCTACGAT GAAGAGGGCG 50  
1 M K R A 4

51 TCCGCTGGAG GGAGCCGGCT GCTGGCATGG GTGCTGTGGC TGCAGGCCTG 100  
5 S A G G S R L L A W V L W L Q A W 21

101 GCAGGTGGCA GCCCCATGCC CAGGTGCCTG CGTATGCTAC AATGAGCCA 150  
22 Q V A A P C P G A C V C Y N E P K 38

151 AGGTGACGAC AAGCTGCCCG CAGCAGGGCC TGCAAGCTGT GCCCCGTGGC 200  
39 V T T S C P Q Q G L Q A V P V G 54

201 ATCCCTGCTG CCAGCCAGCG CATCTTCCTG CACGGCAACC GCATCTCGCA 250  
55 I P A A S Q R I F L H G N R I S H 71

251 TGTGCCAGCT GCCAGCTTCC GTGCCTGCCG CAACCTCACCC ATCCTGTGGC 300  
72 V P A A S F R A C R N L T I L W L 88

301 TGCACTCGAA TGTGCTGGCC CGAATTGATG CGGCTGCCCT CACTGGCCTG 350  
89 H S N V L A R I D A A A F T G L 104

351 GCCCTCCTGG AGCAGCTGGA CCTCAGCGAT AATGCACAGC TCCGGTCTGT 400  
105 A L L E Q L D L S D N A Q L R S V 121

401 GGACCCCTGCC ACATTCCACG GCCTGGGCCG CCTACACACG CTGCACCTGG 450  
122 D P A T F H G L G R L H T L H L D 138

451 ACCGCTGCCGG CCTGCAGGAG CTGGGCCCGG GGCTGTTCCG CGGCCTGGCT 500  
139 R C G L Q E L G P G L F R G L A 154

501 GCCCTGCAGT ACCTCTACCT GCAGGACAAC GCGCTGCAGG CACTGCCTGA 550  
155 A L Q Y L Y L Q D N A L Q A L P D 171

551 TGACACCTTC CGCGACCTGG GCAACCTCAC ACACCTCTTC CTGCACGGCA 600  
172 D T F R D L G N L T H L F L H G N 188

**FIG. 1A**

601 ACCGCATCTC CAGCGTGCC GAGCGCGCCT TCCGTGGCT GCACAGCCTC 650  
189 R I S S V P E R A F R G L H S L 204

651 GACCGTCTCC TACTGCACCA GAACCGCGTG GCCCATGTGC ACCCGCATGC 700  
205 D R L L L H Q N R V A H V H P H A 221

701 CTTCCGTGAC CTTGGCCGCC TCATGACACT CTATCTGTTT GCCAACAAATC 750  
222 F R D L G R L M T L Y L F A N N L 238

751 TATCAGCGCT GCCCACTGAG GCCCTGGCCC CCCTGCCTGC CCTGCAGTAC 800  
239 S A L P T E A L A P L R A L Q Y 254

801 CTGAGGCTCA ACGACAACCC CTGGGTGTGT GACTGCCGGG CACGCCACT 850  
255 L R L N D N P W V C D C R A R P L 271

851 CTGGGCCTGG CTGCAGAAGT TCCGCGGCTC CTCCCTCGAG GTGCCCTGCA 900  
272 W A W L Q K F R G S S S E V P C S 288

901 GCCTCCCGCA ACGCCTGGCT GGCGTGACC TCAAACGCCT AGCTGCCAAT 950  
289 L P Q R L A G R D L K R L A A N 304

951 GACCTGCAGG GCTGCGCTGT GGCCACCGGC CCTTACCATC CCATCTGGAC 1000  
305 D L Q G C A V A T G P Y H P I W T 321

1001 CGGCAGGGCC ACCGATGAGG AGCCGCTGGG GCTTCCAAG TGCTGCCAGC 1050  
322 G R A T D E E P L G L P K C C Q P 338

1051 CAGATGCCGC TGACAAGGCC TCAGTACTGG AGCCTGGAAG ACCAGCTTCG 1100  
339 D A A D K A S V L E P G R P A S 354

1101 GCAGGCAATG CGCTGAAGGG ACGCGTGCCG CCCGGTGACA GCCCGCCGGG 1150  
355 A G N A L K G R V P P G D S P P G 371

1151 CAACGGCTCT GGCCCACGGC ACATCAATGA CTCACCCATT GGGACTCTGC 1200  
372 N G S G P R H I N D S P F G T L P 388

**FIG. 1B**

1201 CTGGCTCTGC TGAGCCCCG GCTCACTGCA GTGCGGCCG AGGGCTCCGA 1250  
389 G S A E P P A H C S A A R G L R 404

1251 GCCACCAGGT TCCCCACTTC GGGCCCTCGC CGGAGGCCAG GCTGTTCACG 1300  
405 A T R F P T S G P R R R P G C S R 421

1301 CAAGAACCGC ACCCGCAGCC ACTGCCGTCT GGGCCAGGCA GGCAGCGGGG 1350  
422 K N R T R S H C R L G Q A G S G G 438

1351 GTGGCGGGAC TGGTGACTCA GAAGGCTCAG GTGCCCTACC CAGCCTCACC 1400  
439 G G T G D S E G S G A L P S L T 454

1401 TGCAGCCTCA CCCCCCTGGG CCTGGCGCTG GTGCTGTGGA CAGTGCTTGG 1450  
455 C S L T P L G L A L V L W T V L G 471

1451 GCCCTGCTGA CCCCCAGCGG ACACAAGAGC GTGCTCAGCA GCCAGGTGTG 1500  
472 P C \* 473

1501 TGTACATACG GGGTCTCTCT CCACGCCGCC AAGCCAGCCG GGCGGCCGAC 1550

1551 CCGTGGGGCA GGCCAGGCCA GGTCCCTCCCT GATGGACGCC TGCCGCCCGC 1600

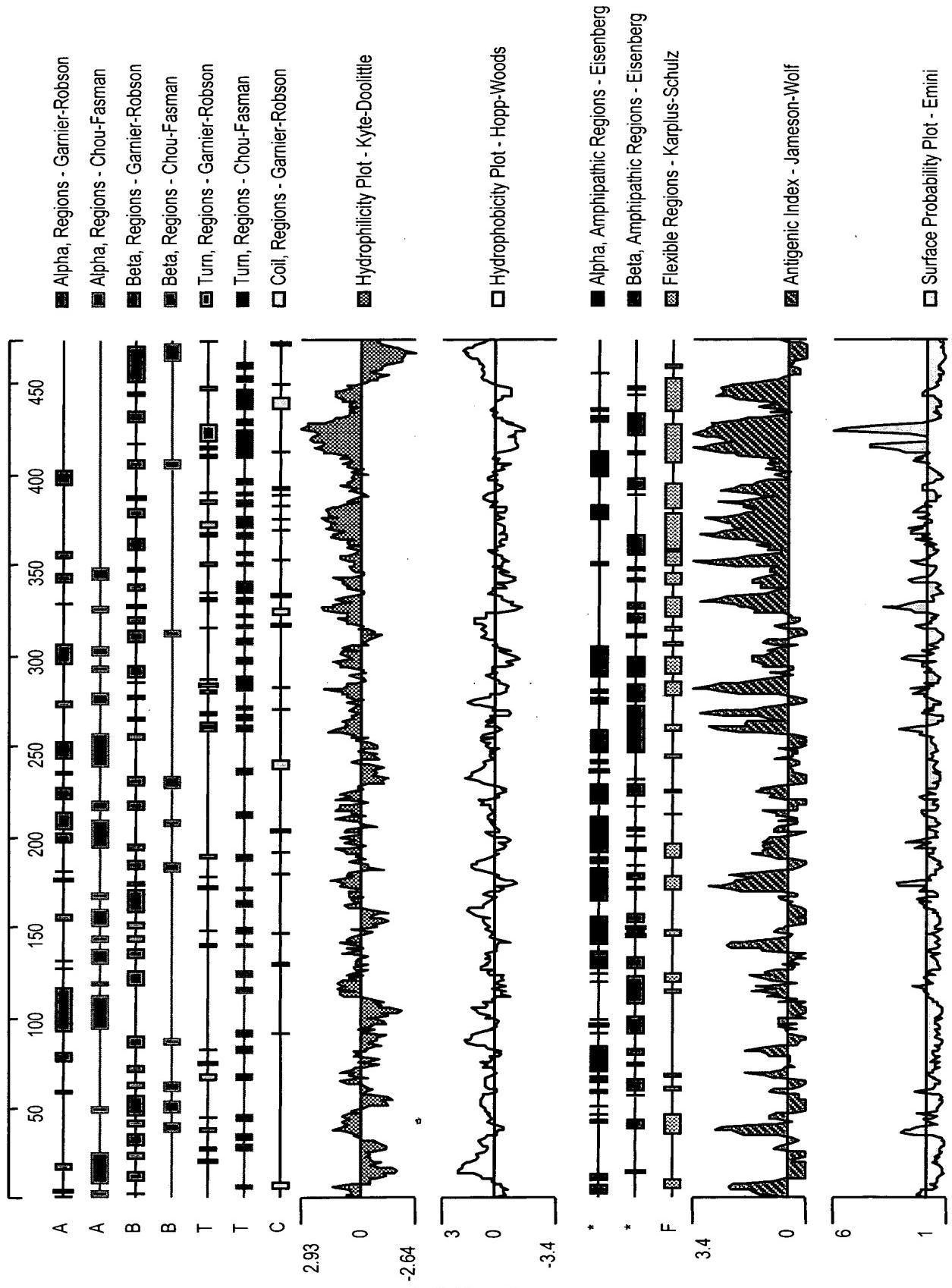
1601 CACCCCCATC TCCACCCCAT CATGTTACA GGGTCGGCG GCAGCGTTG 1650

1651 TTCCAGAACG CCGCCTCCA CCCAGATCGC GGTATATAGA GATATGCATT 1700

1701 TTATTTACT TGTGTAAAAA TATCGGACGA CGTGGAAATAA AGAGCTTTT 1750

1751 TCTTAAAAAA AAAAAAAA AACTCGA 1777

**FIG. 1C**



**FIG. 2**